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Applicant: Kevin L. Gunderson et al.

Examiner: B.J. Forman

Serial No.: 09/394,230

Group Art Unit: 1655

Filed: September 13, 1999

Docket: 1451.003US1

Title: NUCLEIC ACID ANALYSIS USING COMPLETE N-MER ARRAYS

SEP 06 2001
TECH CENTER 1600/2900AMENDMENT AND RESPONSE UNDER 37 C.F.R. § 1.116

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Commissioner for Patents
Washington, D.C. 20231

Applicant has reviewed the Office Action mailed on April 4, 2000. Please amend the above-identified patent application as follows.

IN THE CLAIMS

Please substitute the claim set in the appendix entitled Clean Version of Pending Claims for the previously pending claim set. Specific amendments to individual claims are detailed in the following marked up set of claims.

Please amend the claims as follows:

1. (Twice amended) A method of determining the presence of a mutation in a target polynucleotide, comprising the steps of:
 - (a) providing at least two identical polynucleotide probe arrays, wherein each probe comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each array constitute a complete set of n-mers;
 - (b) hybridizing the target polynucleotide to said overhangs of probe polynucleotides in one array to generate a target hybridization pattern;
 - (c) hybridizing a reference polynucleotide to said overhangs of probe polynucleotides in a second array to generate a reference hybridization pattern; and
 - (d) determining the presence of a mutation in the target polynucleotide by comparing the reference and target hybridization patterns without sequencing the target polynucleotide.
12. (Twice amended) A method of determining whether two or more target polynucleotides are identical without sequencing the target polynucleotides, comprising the steps of: